

Tue Dec 23 10:44:44 2003

us-10-068-238-1.rge

Page 2

SEQ ID NO:1

```
FEATURES             Location/Qualifiers
     source            1..19
                        /organism="synthetic construct"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:32630"
                        /note="Oligonucleotide"
BASE COUNT            8 a      5 c      2 g      4 t
Query Match           100.0%; Score 19; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 8.7;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
ORIGIN
1 CCCAATTGAGTAAACATA 19
|||
1 CCCAATTGAGTAAACATA 19
|||
RESULT 2
LOCUS      BACCAPAB 3244 bp DNA linear BCT 26-APR-1993
DEFINITION B. anthracis encapsulation protein genes (capA, capB, and capC),
complete cds.
ACCESSION M24150.1 GI:142630
VERSION M24150.1
KEYWORDS  encapsulation protein; membrane-associated protein.
SOURCE     Bacillus anthracis
ORGANISM   Bacillus anthracis
            Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus
            cereus group.
            1 (bases 1 to 3244)
REFERENCE 1 Makino, S., Uchida, I., Terakado, N., Sasakawa, C. and Yoshikawa, M.
            Molecular characterization and protein analysis of the cap region,
            which is essential for encapsulation in Bacillus anthracis
            JOURNAL U. Bacteriol. 171 (2), 722-730 (1989)
            MEDLINE 89123146
            PUBMED 2536679
COMMENT     Original source text: B. anthracis (strain TE702; isolate pCAP1)
            DNA.
            Draft entry and computer-readable sequence for [1] kindly provided
            by I. Uchida, 01-MAY-1989.
FEATURES             Location/Qualifiers
     source            1..3244
                        /organism="Bacillus anthracis"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:1392"
                        282..1475
                        /note="44 Kd encapsulation protein CapB"
                        /codon_start=1
                        /transl_table=11
                        /protein_id="AA22286.1"
                        /db_xref="GI:142631"
                        /translation="MIFILGICTVLLIYVIGWQRCQKINSIPRNUNINGRST
                        VRLTIGVQKAKYKVTGCTGTSTSRMYTDEQPIKRRKRGPIGQKRVYKKA
                        DIAEALICECAVDPDYOITFQNMTOANVGVVYLEDHMDWGPPLDVAENFTA
                        TIFNGHLVYIESBIDIFKEVREKRTKIVADNSKISEPLRKTDVWPFQNSLA
                        LAVAEALGIDSEAFRGMKNAIPDGAATFIRPADSKPAFFVNGAANDPSTLRIM
                        ERVYDFGNSLAPIVATMCRPDPRDTEQFARDVLPYKAEIVIAIGETTAITSAFE
                        KSDIPTEQYWNLEGSTSEINRMPYKNIIVYGVNIGAAEPLDIMEQIGKK
                        QAVYI"
     CDS              1490..1939
                        /note="16 Kd encapsulation protein CapC"
                        /codon_start=1
                        /transl_table=11
                        /protein_id="AA22287.1"
                        /db_xref="GI:142632"
                        /translation="MRGSDLYALVLTSTSLITERTGILPAGLVPGYALVNPQ
                        VPMVLPFISLIVYVITGVSRFVILGRKRPATITGICLPLDFCYFVMPFEI
                        FERRSGIVVPGIANTIORQGLPITITLLSGAFATAMNIYLF"
     CDS              1951..3186
                        /note="46 Kd encapsulation protein CapA"
                        /codon_start=1
```

```
FEATURES             Location/Qualifiers
     source            1..94829
                        /organism="Bacillus anthracis str. A2012"
                        /mol_type="genomic DNA"
                        /strain="A2012"
                        /db_xref="taxon:191218"
                        /plasmid="pX02"
                        /note="Florida strain"
                        /complement(543..1139)
                        /gene="BX80001"
                        /complement(543..1139)
                        /gene="BX80001"
                        /note="identified by Glimmer2; putative"
                        /codon_start=1
                        /transl_table=11
                        /product="hypothetical protein, (pX02-03)"
                        /protein_id="AA226162.1"
                        /db_xref="GI:20520281"
                        /translation="MTYVCLPFRSNGQHDVIDPQRPQPEYREADVIRHAIYLD
                        EKKEGQGDVSLKREVKDKCSVNTRKQMDVLKLNELLIAQGSNSLSKEQ
                        EVKSIASVTKSEKGPRTYKREPIENQHORLQREVKYTSFVKKPLPMITDV
                        QIVKKQPHQVPTKIGTGYOIEIMQIPEHRRKELE"
                        complement(1151..1438)
     gene             gene
     CDS              1490..1939
                        /note="16 Kd encapsulation protein CapC"
                        /codon_start=1
                        /transl_table=11
                        /protein_id="AA22287.1"
                        /db_xref="GI:142632"
                        /translation="MRGSDLYALVLTSTSLITERTGILPAGLVPGYALVNPQ
                        VPMVLPFISLIVYVITGVSRFVILGRKRPATITGICLPLDFCYFVMPFEI
                        FERRSGIVVPGIANTIORQGLPITITLLSGAFATAMNIYLF"
     CDS              1951..3186
                        /note="46 Kd encapsulation protein CapA"
                        /codon_start=1
```

gene

SEQ 10 NO:2

```

FEATURES
  source
    Location/Qualifiers
      1..18
        /organism="synthetic construct"
        /mol_type="genomic DNA"
        /db_xref="taxon:32630"
        /note="Oligonucleotide"
BASE COUNT
  7 a 6 c 1 g 4 t
Query Match
  Best Local Similarity 100.0%; Score 18; DB 6; Length 18;
  Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy
  1 ACTGCCATACATTCACAA 18
  1 ACTGCCATACATTCACAA 18
Db
  1 ACTGCCATACATTCACAA 18

RESULT 2
BACCAPAB/C
LOCUS
  BACCAPAB/C 3244 bp DNA linear BCT 26-APR-1993
DEFINITION
  B. anthracis encapsulation protein genes (capA, capB, and capC),
  complete cds.
ACCESSION
  M24150
VERSION
  M24150.1 GI:142630
KEYWORDS
  encapsulation protein; membrane-associated protein.
SOURCE
  Bacillus anthracis
ORGANISM
  Bacillus anthracis
  Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus
  cereus group.
  1 (bases 1 to 3244)
  Makino, S., Uchida, I., Terakado, N., Sasakawa, C. and Yoshikawa, M.
  Molecular characterization and protein analysis of the cap region,
  which is essential for encapsulation in Bacillus anthracis
  J. Bacteriol. 171 (2), 722-730 (1989)
  89123146
  2536679
  Original source text: B. anthracis (strain TE702; isolate pCAP1)
  DNA.
  Draft entry and computer-readable sequence for [1] kindly provided
  by I. Uchida, 01-MAY-1989.
  Location/Qualifiers
    1..3244
      /organism="Bacillus anthracis"
      /mol_type="genomic DNA"
      /db_xref="taxon:1392"
      282..1475
        /note="44 Kd encapsulation protein CapB"
        /codon_start=1
        /transl_table=11
        /protein_id="AAA22286.1"
        /db_xref="GI:142631"
        /translation="MTFTIGTCTVLLIYGVWEDRCQKRLNIPFIVNIRGKST
        VRLITGVQAKRYKTVGKTGTSTAKMTYMTDGEQPIKRKEGPNIGEORAVVKEA
        DLAEALICECAVOPDYCIIFONMIOANQVAVNVLEDMWGPFLBVEVAFA
        TTPYNGHLVITSEVLYDFKEVAERNTKVIADNSRISSEFLKRPDYMFPDASIA
        LAVAALGIDETAFRGMNAHPDGAARITRFAPQSKAFVNGFPAANDPSSSLRA
        ERYVDGYSNLAIVTAMNCRPRVDRTEOPARDVLPYKAEIVAIAGETTAPITSAR
        KGDIPQERVNLSEGSTSEISMREAPYKNTKIVGVGNTHAAEPLIDMEIDICK
        QAKVT"
        1490..1939
          /note="16 Kd encapsulation protein CapC"
          /codon_start=1
          /transl_table=11
          /protein_id="AAA22287.1"
          /db_xref="GI:142632"
          /translation="MKGSDIYAIIVAGVTLSTFTERTGIIIPAGLVVPGYAIIVNOP
          VFMVLVPTISILTYIVTVYGVSRPMILIGRRKFAATLTGTGCLALPDYCPVWPFBI
          FERRIGVIVPGIANTIQGLPLTIGTTLDSGATFALNNIYLLF"
          1951..3186
            /note="46 Kd encapsulation protein CapA"
            /codon_start=1

FEATURES
  source
    Location/Qualifiers
      1..94829
        /organism="Bacillus anthracis str. A2012"
        /mol_type="genomic DNA"
        /strain="A2012"
        /db_xref="taxon:191218"
        /plasmid="pX02"
        /note="Florida strain"
        /complement(543..1139)
        /gene="BXB0001"
        /complement(543..1139)
        /gene="BXB0001"
        /complement(543..1139)
        /note="identified by Glimmer2; putative"
        /codon_start=1
        /transl_table=11
        /product="hypothesized protein, (pX02-03)"
        /protein_id="AAM26162.1"
        /db_xref="GI:20520281"
        /translation="MTYVKLPQFGNGNIHVDVDDPQVPEYVREADVLRHATVLD
        EMERKQDDVSLIKKEVVDKRSVNTMCAQMDVLKAMELLAAGSGSLSEKLEQ
        EVKSEIASVTKSEGRPRVTRKPLEENVOEHQIQREVKITTSFVKELPMTTDDY
        QIVMKGRPHGVPTFRLTGTGQIELEWQIEHRRKELDE"
        complement(1151..1438)

```

FEATURES and Research (US)  
Location/Qualifiers  
source 1. .32  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:33630"  
/note="oligonucleotide"

BASE COUNT 11 a 7 c 7 g 7 t

Query Match 100.0%; Score 32; DB 6; Length 32;  
Best Local Similarity 100.0%; Pred. No. 0.00087;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGATTAGCGCCGTAAGAAGTCTTATATC 32  
1 CGATTAGCGCCGTAAGAAGTCTTATATC 32

RESULT 2  
BACCAPAC  
LOCUS 3244 bp DNA linear BCT 26-Apr-1993  
DEFINITION B. anthracis encapsulation protein genes (capA, capB, and capC),  
complete cds.  
ACCESSION M24150.1 GI:142630  
VERSION M24150.1  
KEYWORDS encapsulation protein; membrane-associated protein.  
SOURCE Bacillus anthracis  
ORGANISM Bacillus anthracis  
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus  
cereus group.  
1 (bases 1 to 3244)  
Makino, S., Uchida, I., Terakado, N., Sasakawa, C. and Yoshikawa, M.  
Molecular characterization and protein analysis of the cap region,  
which is essential for encapsulation in Bacillus anthracis  
J. Bacteriol. 171 (2), 722-730 (1989)  
JOURNAL 89123146  
MEDLINE 2536679  
PUBMED  
COMMENT Original source text: B. anthracis (strain 78702; isolate pCAP1)  
DNA  
Draft entry and computer-readable sequence for [1] kindly provided  
by I. Uchida, 01-May-1989.  
Location/Qualifiers  
1. .3244  
/organism="Bacillus anthracis"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:1392"  
282\_1475  
/note="44 Kd encapsulation protein CapB"  
/codon\_start=1  
/transl\_table=11  
/protein\_id="AA22286.1"  
/db\_xref="GI:142631"  
/translation="MIFIGICTVFLIYGIWECHOKRLNSIPIRVNINGIKRST  
VRLITGVQEAQYKVTGKTSAMTYWDEOPIKRREGNIGBORVYKKA  
DLEAEALICEQAVQDYOILFONMIOANVATVNEEDMDWGPDLDAVAFPA  
TTPYNGHIVTISEYLDYKFEVAREKNTVYVAGVATSEELIKRPPMDPDAKA  
LVAEALGIDEETAFRGMNAHPDPGAKRITFPADQSPAFVNGFANDSSLRIN  
ERVDDFGISNLAVITMNCRPRVDRTEOPADVPYKAEIVLIGTTAPITSAE  
KGDIPTEQWNLGEMSTSEIMSRMYLKNRLVYGVGNIHGAAPLIDIMEQIGKK  
QAKVI"  
1490. .1939  
/note="16 Kd encapsulation protein CapC"  
/codon\_start=1  
/transl\_table=11  
/protein\_id="AA22287.1"  
/db\_xref="GI:142632"  
/translation="MFGSDYLALVGLTSLIFETRGILPAGLVGVGLAVLNPQ  
VFMVLVFLISILYVIVYGVSRFMLYGRKFAATLITGICLKLFPYCYVPMPEI  
FERRGIGVIVPGIANTIORGLPLITGITLLSGATFAMNMYL"  
1951. .3186  
/note="46 Kd encapsulation protein CapA"  
/codon\_start=1

FEATURES and Research (US)  
Location/Qualifiers  
source 1. .32  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:33630"  
/note="oligonucleotide"

BASE COUNT 1120 a 458 c 697 g 969 t

Query Match 100.0%; Score 32; DB 1; Length 3244;  
Best Local Similarity 100.0%; Pred. No. 0.00075;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGATTAGCGCCGTAAGAAGTCTTATATC 32  
523 CGATTAGCGCCGTAAGAAGTCTTATATC 554

RESULT 3  
AB011191/c  
LOCUS 94829 bp DNA circular BCT 14-JUN-2002  
DEFINITION Bacillus anthracis str. A2012 plasmid pX02, complete sequence.  
ACCESSION AB011191  
VERSION AB011191.1 GI:20520280  
KEYWORDS  
SOURCE  
ORGANISM  
Bacillus anthracis str. A2012  
Bacillus anthracis str. A2012  
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus  
cereus group.  
1 (bases 1 to 94829)  
Read, T.D., Salzberrg, S.L., Pop, M., Shumway, M., Umayam, L., Jiang, L.,  
Holzapfel, E., Busch, J.D., Smith, K.L., Schupp, J.M., Solomon, D.,  
Keim, P. and Fraser, C.M.  
Comparative genome sequencing for discovery of novel polymorphisms  
in Bacillus anthracis  
Science 296 (5575), 2028-2033 (2002)  
JOURNAL 12004073  
MEDLINE 22061436  
PUBMED  
COMMENT 2 (bases 1 to 94829)  
Read, T.D., Salzberrg, S.L., Pop, M., Shumway, M., Umayam, L., Jiang, L.,  
Holzapfel, E., Busch, J.D., Smith, K.L., Schupp, J.M., Solomon, D.,  
Keim, P. and Fraser, C.M.  
Direct Submission  
Submitted (09-May-2002) The Institute for Genomic Research, 9712  
Medical Center Dr, Rockville, MD 20850, USA  
Location/Qualifiers  
1. .94829  
/organism="Bacillus anthracis str. A2012"  
/mol\_type="genomic DNA"  
/strain="A2012"  
/db\_xref="taxon:191218"  
/plasmid="pX02"  
/note="Florida strain"  
complement (543. .1139)  
/gene="BXB0001"  
complement (543. .1139)  
/gene="BXB0001"  
/note="identified by Glimmer2; putative"  
/codon\_start=1  
/transl\_table=11  
/product="hypothetical protein, (pX02-03)"  
/protein\_id="AA26162.1"  
/db\_xref="GI:20520281"  
/translation="MTYVKLFQFQNGQIHVDIVQDFQRYEYFREADVLRHAIYLD  
EXMRGKQDDVSLIKKEVKDLKOSVQKQMDVLILKMLLEIAGSGNSLSKLEQ  
EYKSIASVTKSEKGFPTVREPEILENVQEHQRIQREVKTISFVKKPLPWITDV  
QIVMKKGPHQVVPRLQGTGYQBIEMEQIEHRRKELE"  
complement (1151. .1438)

CEQ 10 NOV 03

Tue Dec 23 10:44:55 2003

us-10-068-238-4.rge

Page 2

SEQ ID NO:4

FEATURES  
and Research (US)  
Location/Qualifiers

source

1..30

/organism="synthetic construct"

/mol\_type="genomic DNA"

/db\_xref="taxon:32630"

/note="Oligonucleotide"

9 a 4 c 12 g 5 t

BASE COUNT

ORIGIN

Query Match

Best Local Similarity 100.0%; Score 30; DB 6; Length 30;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GTGAGCAACGACGGGTAGTTAAAGAGCGTG 30

1 GTGAGCAACGACGGGTAGTTAAAGAGCGTG 30

RESULT 2

BACCAPAC

LOCUS

DEFINITION

complete cds.

VERSION

KEYWORDS

SOURCE

ORGANISM

Bacillus anthracis

Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus

cereus group.

1 (bases 1 to 3244)

Makino, S., Uchida, I., Terakado, N., Sasakawa, C. and Yoshikawa, M.

Molecular characterization and protein analysis of the cap region,

which is essential for encapsulation in Bacillus anthracis

J. Bacteriol. 171 (2), 722-730 (1989)

89123146

2536679

JOURNAL

MEDLINE

PUBMED

COMMENT

DNA.

Draft entry and computer-readable sequence for [1] kindly provided

by I. Uchida, 01-MAY-1989.

Location/Qualifiers

1..3244

/organism="Bacillus anthracis"

/mol\_type="genomic DNA"

/db\_xref="taxon:1392"

282..1475

/note="44 Kd encapsulation protein CapB"

/codon\_start=1

/transl\_table=1

/protein\_id="AA02286.1"

/db\_xref="GI:142631"

/translation="MTFTIGCTVFLIIVGIMBQCRKLNSIPIRVINGIRGKST

VTRLITGVQEAQKVTGKTTGSAKMTIWTDEBPQIKRKEGPNIGQRVVKKAA

DLKALICBMAVQDYOIIFQKMIQAVGVVNLJEDHVMGPTLDEVAEATA

TIPTNGHLVITSEYLDYFKVEAEKTVIVADNSRISEEPKRPDVFVFNASTA

LAVKALGIDETAFRGLNANPDRGMRITRPADSKKAPFNGSPANDPSSITLAI

ERVDPRGYSNAPIVIMNCRDPRDRTEQARVDLPITKAEIVTAIGETAPITSAFE

KGDIPTDFYMLBGMSTSEIWSRMRPYLKNRIYGVGNHGAEPFLDMIMEQISIK

QAKYI"

1490..1939

/note="16 Kd encapsulation protein CapC"

/codon\_start=1

/transl\_table=1

/protein\_id="AA02287.1"

/db\_xref="GI:142632"

/translation="WFGSDIYIALVLGVLTSLIFTEGTGLPAGLVVPGYALVFNOP

VPMVLVFLISILVIVTVGVSRFMILYGRKRPATLITGICLILFDYCYPMPEI

FEFGIGVIVPGLIANTIQOGLPLITGTLILSGAFAIMNIYILF"

1951..3186

/note="46 Kd encapsulation protein CapA"

/codon\_start=1

gene

Query Match

Best Local Similarity 100.0%; Score 30; DB 1; Length 3244;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GTGAGCAACGACGGGTAGTTAAAGAGCGTG 30

1 GTGAGCAACGACGGGTAGTTAAAGAGCGTG 30

RESULT 3

AE011191/c

LOCUS

DEFINITION

complete sequence.

VERSION

KEYWORDS

SOURCE

ORGANISM

Bacillus anthracis str. A2012

Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus

cereus group.

1 (bases 1 to 94829)

Read, T.D., Salzberg, S.L., Pop, M., Shumway, M., Umayam, L., Jiang, L.,

Holtzapfel, E., Busch, J.D., Smith, K.L., Schupp, J.M., Solomon, D.,

Keim, P. and Fraser, C.M.

Comparative genome sequencing for discovery of novel polymorphisms

in Bacillus anthracis

Science 296 (5575), 2028-2033 (2002)

22061436

12004073

JOURNAL

MEDLINE

PUBMED

COMMENT

DNA.

Draft entry and computer-readable sequence for [1] kindly provided

by T. D. Read, 09-MAY-2002 The Institute for Genomic Research, 9712

Medical Center Dr, Rockville, MD 20850, USA

Location/Qualifiers

1..94829

/organism="Bacillus anthracis str. A2012"

/mol\_type="genomic DNA"

/strain="A2012"

/db\_xref="taxon:191218"

/Plasmid="pX02"

/note="Florida strain"

complement (543..1139)

/gene="BX80001"

complement (543..1139)

/note="identified by Glimmer2; putative"

/codon\_start=1

/transl\_table=1

/product="hypothetical protein, (pX02-03)"

/protein\_id="AA02162.1"

/db\_xref="GI:20520281"

/translation="MTYVKLPQPGNGNIHVDIVDDPQRYPEYPRADVTRHAIYLD

EKMREGQDDVSLKKEVCDLQSVITKQMDVLTKMELIAQSGSNLSLEKQ

EVSEIASVTKSEKFPRTVREPELEENVOEQRQIKREVKTSFVKKPLPMITDVO

QIVKKKPHQVPTRLGTGVOELWQIEPHEKKELE"

complement (1151..1438)

gene

SEQ ID NO:5

NAODFESTPTITMNYNOFLEKTKOLRLPTDOYGNATATYFENRVRUDGNSMSE  
 VLPOIOETIARIIPNGKDLNIVERRIAANVSPDLERETKALAKIAEFGNEN  
 GNLOYOQKDLTEFPNFDQOOSNINQKQALBELNATNITYLVDKIKNAKNILIRK  
 FHYDRNNIAVAGADSVVKAHREYVINSSTGGLNIDKDKIRKILSGIYEIEDTEBK  
 EVINDRYDMNINISLRQDKTFIDFKYKNDKPLIYISNPNYKVVAVATMENTIINPS  
 ENGDTSTNGIKKILIFSKGGEIG"

BASE COUNT 924 a 338 c 441 g 666 t

ORIGIN

Query Match 100.0%; Score 19; DB 1; Length 2369;  
 Best Local Similarity 100.0%; Pred. No. 8.4;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 TACAGACGAGTGTATAG 19  
 |||||  
 852 TACAGACGAGTGTATAG 870

RESULT 12  
 AF306779  
 LOCUS 2369 bp DNA linear BCT 13-DEC-2000  
 DEFINITION Bacillus anthracis isolate 28 protective antigen (pag) gene,  
 complete cds.  
 ACCESSION AF306779  
 VERSION AF306779.1 GI:10880944  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Bacillus anthracis  
 Bacillus anthracis  
 Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus  
 cereus group.

REFERENCE 1 (bases 1 to 2369)  
 PRICE, L.B., Hugh-Jones, M., Jackson, P.J. and Keim, P.  
 Genetic diversity in the protective antigen gene of *Bacillus anthracis*  
 J. Bacteriol. 181 (8), 2358-2362 (1999)  
 JOURNAL 99214082  
 MEDLINE 10197996  
 PUBLISHED 2 (bases 1 to 2369)  
 REFERENCE PRICE, L.B., Hugh-Jones, M., Jackson, P.J. and Keim, P.  
 Direct Submission  
 Submitted (20-SEP-2000) Biological Sciences, Northern Arizona  
 University, P.O. Box 5640, Flagstaff, AZ 86011-5640, USA  
 JOURNAL  
 TITLE  
 JOURNAL  
 FEATURES  
 source  
 1..2369  
 location/Qualifiers  
 /organism="Bacillus anthracis"  
 /mol\_type="other DNA"  
 /isolate="28"  
 /db\_xref="taxon:1392"  
 /plasmid="pX01"  
 1..2369  
 /gene="pag"  
 49..2343  
 /gene="pag"  
 /codon\_start=1  
 /transl\_table=1  
 /product="protective antigen"  
 /protein\_id="AAG24447.1"  
 /db\_xref="GI:10880944"  
 /translation="MKRRKVLIPMALSTILVSTGNLEVIQAQVKEQENRLNSESSE  
 SQGLAGYFSDNFOAPMVVTSITGDLSPSELENIPEENQYFQSAIWGFIKVK  
 SDEYFATSDNHTVMWVDOEVINKASNSKRIEKGRLVQIOYORENPTKGLD  
 FKLWYTDQNKKEVTSIDNQLPELKQSSNSKRSAGTVPDPNDNGIDSLV  
 EGYVDVYKRTFLSPWISNHEKKGITKYSSEKSTASDPYSDPEKVTGRIDNV  
 SPEARHPLVAAPYIVHVDMENTILSKNEQSTONDSQRTISKNTSRTHTSEVHG  
 NAEYHASFPIGGSVAGFSSNSSTVAIDHSLSLACERTWATMGNTADTARLAN  
 IRYVNTGTAPRYNVLPTTSVLGKQVLATIKAKENQLSLAPNNYPSKNAPIAL  
 NAQDFESTPTITMNYNOFLEKTKOLRLPTDOYGNATATYFENRVRUDGNSMSE  
 VLPOIOETIARIIPNGKDLNIVERRIAANVSPDLERETKALAKIAEFGNEN  
 GNLOYOQKDLTEFPNFDQOOSNINQKQALBELNATNITYLVDKIKNAKNILIRK  
 FHYDRNNIAVAGADSVVKAHREYVINSSTGGLNIDKDKIRKILSGIYEIEDTEBK  
 EVINDRYDMNINISLRQDKTFIDFKYKNDKPLIYISNPNYKVVAVATMENTIINPS  
 ENGDTSTNGIKKILIFSKGGEIG"

gene  
 CDS  
 BASE COUNT 924 a 339 c 441 g 665 t

ORIGIN  
 Query Match 100.0%; Score 19; DB 1; Length 2369;  
 Best Local Similarity 100.0%; Pred. No. 8.4;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 TACAGACGAGTGTATAG 19  
 |||||  
 852 TACAGACGAGTGTATAG 870

RESULT 13  
 AF306780  
 LOCUS 2369 bp DNA linear BCT 13-DEC-2000  
 DEFINITION Bacillus anthracis isolate BAI035 protective antigen (pag) gene,  
 complete cds.  
 ACCESSION AF306780  
 VERSION AF306780.1 GI:10880946  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Bacillus anthracis  
 Bacillus anthracis  
 Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus  
 cereus group.

REFERENCE 1 (bases 1 to 2369)  
 PRICE, L.B., Hugh-Jones, M., Jackson, P.J. and Keim, P.  
 Genetic diversity in the protective antigen gene of *Bacillus anthracis*  
 J. Bacteriol. 181 (8), 2358-2362 (1999)  
 JOURNAL 99214082  
 MEDLINE 10197996  
 PUBLISHED 2 (bases 1 to 2369)  
 REFERENCE PRICE, L.B., Hugh-Jones, M., Jackson, P.J. and Keim, P.  
 Direct Submission  
 Submitted (20-SEP-2000) Biological Sciences, Northern Arizona  
 University, P.O. Box 5640, Flagstaff, AZ 86011-5640, USA  
 JOURNAL  
 TITLE  
 JOURNAL  
 FEATURES  
 source  
 1..2369  
 location/Qualifiers  
 /organism="Bacillus anthracis"  
 /mol\_type="other DNA"  
 /isolate="BAI035"  
 /db\_xref="taxon:1392"  
 /plasmid="pX01"  
 1..2369  
 /gene="pag"  
 49..2343  
 /gene="pag"  
 /codon\_start=1  
 /transl\_table=1  
 /product="protective antigen"  
 /protein\_id="AAG24446.1"  
 /db\_xref="GI:10880947"  
 /translation="MKRRKVLIPMALSTILVSTGNLEVIQAQVKEQENRLNSESSE  
 SQGLAGYFSDNFOAPMVVTSITGDLSPSELENIPEENQYFQSAIWGFIKVK  
 SDEYFATSDNHTVMWVDOEVINKASNSKRIEKGRLVQIOYORENPTKGLD  
 FKLWYTDQNKKEVTSIDNQLPELKQSSNSKRSAGTVPDPNDNGIDSLV  
 EGYVDVYKRTFLSPWISNHEKKGITKYSSEKSTASDPYSDPEKVTGRIDNV  
 SPEARHPLVAAPYIVHVDMENTILSKNEQSTONDSQRTISKNTSRTHTSEVHG  
 NAEYHASFPIGGSVAGFSSNSSTVAIDHSLSLACERTWATMGNTADTARLAN  
 IRYVNTGTAPRYNVLPTTSVLGKQVLATIKAKENQLSLAPNNYPSKNAPIAL  
 NAQDFESTPTITMNYNOFLEKTKOLRLPTDOYGNATATYFENRVRUDGNSMSE  
 VLPOIOETIARIIPNGKDLNIVERRIAANVSPDLERETKALAKIAEFGNEN  
 GNLOYOQKDLTEFPNFDQOOSNINQKQALBELNATNITYLVDKIKNAKNILIRK  
 FHYDRNNIAVAGADSVVKAHREYVINSSTGGLNIDKDKIRKILSGIYEIEDTEBK  
 EVINDRYDMNINISLRQDKTFIDFKYKNDKPLIYISNPNYKVVAVATMENTIINPS  
 ENGDTSTNGIKKILIFSKGGEIG"

gene  
 CDS  
 BASE COUNT 924 a 337 c 441 g 667 t

ORIGIN  
 Query Match 100.0%; Score 19; DB 1; Length 2369;  
 Best Local Similarity 100.0%; Pred. No. 8.4;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 TACAGACGAGTGTATAG 19  
 |||||  
 1 TACAGACGAGTGTATAG 19

VERSION AJ413936.1 GI:16031492  
 KEYWORDS pag gene  
 SOURCE Bacillus anthracis  
 ORGANISM Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.

REFERENCE 1  
 Adone, R., Pasquali, P., La Rosa, G., Marianelli, C., Muscillo, M., Fasanella, A., Francia, M. and Ciuchini, F.  
 Sequence analysis of the gene encoding for the major virulence factors of bacillus anthracis vaccine strain 'Carbosap 2' (bases 1 to 2231)  
 J. Appl. Microbiol. 92, 1-5 (2002)

REFERENCE 2  
 Muscillo, M.  
 Direct Submission  
 Submitted (11-SEP-2001) Muscillo M., Environmental Hygiene, Istituto Superiore di Sanita, Viale Regina Elena 299, Rome 00199, Italy

FEATURES  
 source  
 1..2231  
 /location/Qualifiers  
 /organism="Bacillus anthracis"  
 /mol\_type="genomic DNA"  
 /strain="Carbosap"  
 /isolate="IT-Carb3-6254"  
 /db\_xref="taxon:1392"  
 /plasmid="pX01"  
 /country="Italy"  
 /note="vaccine against anthrax in cattle and sheep"

gene  
 1..2231  
 /gene="pag"  
 <1..>2231  
 /gene="pag"  
 /function="protective antigen"  
 /codon\_start=2  
 /transl\_table=11  
 /product="Pag protein"  
 /protein\_id="CAC93934.1"  
 /db\_xref="GI:16031493"  
 /db\_xref="SPRMBL:Q937W3"  
 /translation="PLMALSTILVSTGNLEVIQAEVKOENRLNESSESSOGILGY FSDINFOAPVAVTSTGDISSSELENIPSENOYFOSAIWSGPIKYKSDPEYFAT SADNHTWMDQEVNKAASNKIRLEKGYOIKYQRENPEKGDIFLYTDS QNKREIVSSDNOLPELKOKSSNRKSTAGPTVPRDNDGIPDSLEVBGITVDK NKRTPLSPWISNHEKGLTKYKSPKSTASDPYSDKVTGRIDKXVSEAHPL VAAVPIVHVDMMNIILSKNEDOSTONTDQRTISKNTSRTHTSEVAGNAEVASF FDIGSVSAGFNSNSVVAIDHSLSLAERTWAEWTMGANTADTLRLNANIEYVGT APIYVNLPTTSILVIGKNOQLATIKAKENOLSOILAPNNYPSKNLAPIALNADDFSS TPTTNVNOFLELEKTKOQLDIDOVGNIAATFNENGVAVDTSNMSEVLPJOIQT TARIIFNGDNLVERIRIAVNSDPLETTKDPMLKALKTAFGNENGLDYCK DTEPDPNDOOTSONIKOIAELANTNTYTLDKIKANAKNILLIRDKRPHYDRNT AVGADSVKAEARVINSSTBELNIDNDIKRISGIVIEIDEBGKKEVINRIYD MNTISSRQDGKTFIDFKKNDKPLIYISNPYKXNVAVAKENTTINSENGDTSTN GIK"

BASE COUNT 861 a 328 c 422 g 620 t

ORIGIN

Query Match 100.0%; Score 18; DB 1; Length 2231;  
 Best Local Similarity 100.0%; Pred. No. 1e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 TTTCAGCCCAAGTCTTT 18  
 Db 1109 TTTCAGCCCAAGTCTTT 1092

RESULT 10  
 AF306778/c  
 LOCUS AF306778 2369 bp DNA linear BCT 13-DEC-2000  
 DEFINITION Bacillus anthracis plasmid pX01 protective antigen (pag) gene,  
 complete cds.  
 ACCESSION AF306778  
 VERSION AF306778.1 GI:10880942  
 KEYWORDS

SOURCE  
 ORGANISM Bacillus anthracis  
 Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.

REFERENCE 1  
 Price, L.B., Hugh-Jones, M., Jackson, P.J. and Keim, P.  
 Genetic diversity in the protective antigen gene of Bacillus anthracis  
 J. Bacteriol. 181 (8), 2358-2362 (1999)

REFERENCE 2  
 Price, L.B., Hugh-Jones, M., Jackson, P.J. and Keim, P.  
 Direct Submission  
 Submitted (20-SEP-2000) Biological Sciences, Northern Arizona University, P.O. Box 5640, Flagstaff, AZ 86011-5640, USA

FEATURES  
 source  
 1..2369  
 /location/Qualifiers  
 /organism="Bacillus anthracis"  
 /mol\_type="other DNA"  
 /db\_xref="taxon:1392"  
 /plasmid="pX01"  
 1..2369  
 /gene="pag"  
 49..2343  
 /gene="pag"  
 /codon\_start=1  
 /transl\_table=11  
 /product="protective antigen"  
 /protein\_id="AAG24446.1"  
 /db\_xref="GI:10880943"  
 /translation="MKKKRVILPIMASTLIVSTGNLEVIQAEVKOENRLNESSESSOGILGYFSDINFOAPVAVTSTGDISSSELENIPSENOYFOSAIWSGPIKYKSDPEYFAT SADNHTWMDQEVNKAASNKIRLEKGYOIKYQRENPEKGDIFLYTDS QNKREIVSSDNOLPELKOKSSNRKSTAGPTVPRDNDGIPDSLEVBGITVDK NKRTPLSPWISNHEKGLTKYKSPKSTASDPYSDKVTGRIDKXVSEAHPL VAAVPIVHVDMMNIILSKNEDOSTONTDQRTISKNTSRTHTSEVAGNAEVASF FDIGSVSAGFNSNSVVAIDHSLSLAERTWAEWTMGANTADTLRLNANIEYVGT APIYVNLPTTSILVIGKNOQLATIKAKENOLSOILAPNNYPSKNLAPIALNADDFSS TPTTNVNOFLELEKTKOQLDIDOVGNIAATFNENGVAVDTSNMSEVLPJOIQT TARIIFNGDNLVERIRIAVNSDPLETTKDPMLKALKTAFGNENGLDYCK DTEPDPNDOOTSONIKOIAELANTNTYTLDKIKANAKNILLIRDKRPHYDRNT AVGADSVKAEARVINSSTBELNIDNDIKRISGIVIEIDEBGKKEVINRIYD MNTISSRQDGKTFIDFKKNDKPLIYISNPYKXNVAVAKENTTINSENGDTSTN GIK"

BASE COUNT 924 a 338 c 441 g 666 t

ORIGIN

Query Match 100.0%; Score 18; DB 1; Length 2369;  
 Best Local Similarity 100.0%; Pred. No. 1e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 TTTCAGCCCAAGTCTTT 18  
 Db 1180 TTTCAGCCCAAGTCTTT 1163

RESULT 11  
 AF306779/c  
 LOCUS AF306779 2369 bp DNA linear BCT 13-DEC-2000  
 DEFINITION Bacillus anthracis isolate 28 protective antigen (pag) gene,  
 complete cds.  
 ACCESSION AF306779  
 VERSION AF306779.1 GI:10880944  
 KEYWORDS  
 SOURCE Bacillus anthracis  
 ORGANISM Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.

REFERENCE 1  
 Price, L.B., Hugh-Jones, M., Jackson, P.J. and Keim, P.  
 Genetic diversity in the protective antigen gene of Bacillus anthracis

REFERENCE	KEYWORDS	ORGANISM	REFERENCE	KEYWORDS	ORGANISM
1	Adone, R., Paeguali, P., La Rosa, G., Marianelli, C., Muscillo, M., Rasmella, A., Franca, M. and Cinchini, P.	Bacillus anthracis	2	Sequence analysis of the gene encoding for the major virulence factors of <i>Bacillus anthracis</i> vaccine strain 'Carposap'	<i>Bacillus anthracis</i>
3	J. Appl. Microbiol. 92, 1-5 (2002)		4	(bases 1 to 231)	
5	Muscillo, M.		6	Direct Submission	
7	Submitted (11-SEP-2001)		8	Muscillo M., Environmental Hygiene, Istituto Superiore di Sanita, Viale Regina Elena 299, Rome 00199, Italy	

```
gene      1. .2231
          /gene="pag"
CDS       <1. .>2231
```

BASE COUNT	861 a	328 c	422 g	620 f
ORIGIN				

Query Match	100.0%;	Score 22;	DB 1;	Length 2231;
Best Local Similarity	100.0%;	Pred. No. 4.6;		
Matches 22;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

```

QY      1 AGTACATGGAATGCAGAAGTG 22
          |||||
DB      970 AGTACATGGAATGCAGAAGTG 991

```

RESULT 10)	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS
AF306778	AF306778	2369 bp DNA linear BCR 13-DEC-2000			
		<i>Bacillus anthracis</i> plasmid pX01 protective antigen (pag) gene, complete cds.			
			AF306778		
			AF306778.1	GI:10880942	

SOURCE	ORGANISM
REFERENCE	<i>Bacillus anthracis</i>
AUTHORS	<i>Bacillus anthracis</i>
TITLE	Bacteria; Firmicutes; Bacillales; Bacillaceae; <i>Bacillus</i> ; <i>Bacillus</i>
JOURNAL	cereus group.
MEDLINE	1 (bases 1 to 2369)
PUBMED	Price, L.B., Hugh-Jones, M., Jackson, P.J., and Keim, P.
AUTHORS	Genetic diversity in the protective antigen gene of <i>Bacillus</i>
TITLE	<i>anthracis</i>
JOURNAL	<i>J. Bacteriol.</i> 181 (8), 2358-2362 (1999)
FEATURES	99214082
source	10197996
	2 (bases 1 to 2369)
	Price, L.B., Hugh-Jones, M., Jackson, P.J., and Keim, P.
	Direct Submission
	Submitted (20-SEP-2000) Biological Sciences, Northern Arizona
	University, P.O. Box 5640, Flagstaff, AZ 86011-5640, USA
	Location/Qualifiers
	1
	2369
	location="Bacillus anthracis"

gene  
CDS

BASE COUNT	.924	a	338	c	441	g	666	t
ORIGIN								

Query Match	100.0%;	Score 22;	DB 1;	Length 2369;
Best Local Similarity	100.0%;	Pred. No. 4.7;		
Matches 22;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

```

QY      1 AGTACATGGAATGCAGAGTG  22
        |||||
Db      1041 AGTACATGGAATGCAGAGTG 1062

```

RESULT 11	AF306779	2369 bp	DNA	linear	BCR 13-DEC-2000
LOCUS	AF306779				
DEFINITION	Bacillus anthracis isolate 28 protective antigen (pag) gene,				
ACCESSION	AF306779				
VERSION	AF306779.1				
KEYWORDS	complete cds.				
SOURCE	Bacillus anthracis				
ORGANISM	Bacillus anthracis				
REFERENCE	1 (bases 1 to 2369)				
AUTHORS	Price, L.R., Hugh-Jones, M., Jackson, P.J. and Keim, P.				
TITLE	Genetic diversity in the protective antigen gene of Bacillus anthracis				



VERSION	AJ41936.1	GI:16031492
KEYWORDS	pag gene.	
SOURCE	Bacillus anthracis	
ORGANISM	Bacillus anthracis	
	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus	
	Cereus group.	
REFERENCE	1	
AUTHORS	Adone, R., Paequali, P., La Rosa, G., Marianielli, C., Muscillo, M., Pasanello, A., Francia, M., and Ciuchini, F.	
TITLE	Sequence analysis of the gene encoding for the major virulence factors of bacillus anthracis vaccine strain 'Carbosap'	
JOURNAL	J. Appl. Microbiol. 92, 1-5 (2002)	
REFERENCE	2 (bases 1 to 2231)	
AUTHORS	Muscillo, M.	
TITLE	Direct Submission	
JOURNAL	Submitted (11-SEP-2001) Muscillo M., Environmental Hygiene, Istituto Superiore di Sanita, Viale Regina Elena 299, Rome 00199, Italy	
FEATURES	source	
	1..2231	
	/location="Qualifiers"	
	/organism="Bacillus anthracis"	
	/mol_type="genomic DNA"	
	/strain="Carbosap"	
	/isolate="IT-Carbs-6254"	
	/db_xref="taxon:1392"	
	/plasmid="PX01"	
	/country="Italy"	
	/note="vaccine against anthrax in cattle and sheep"	
gene	1..2231	
	/gene="pag"	
CDS	<1..>2231	
	/gene="pag"	
	/function="protective antigen"	
	/codon_start=2	
	/transl_table=11	
	/product="Pag protein"	
	/protein_id="CA03943.1"	
	/db_xref="GI:16031493"	
	/db_xref="SPTRMBU:Q937M3"	
	/translation="PLMALSTILVSTGNTLEVLQAQEVKQENRLNEBSBSOGILLGYVY FSDLPQAPMVAVTSSTGTDLISPESELENIPSENQFSAIWSQFIKKXSDDEVATPAT SADNIVTMVDQDEVIINKASNSNKIRLEKGLLYQKIQYQRENPTKEGLDPKLWMTDSS ONKNEVVISDNLOLPELKOKXSNSRKRSKTAGPVPVRKDNGIPIIDSLVEGVYADVAK NKRTLSPMWISNIHEKGLTYKKSPEKMSASTASDPSEFEKVORIDKVAEPEARHPLPL VAAVYIVHVDMENTIIISKNOPOSOTMDSORRTISKNTSRTHTSEHGNAEVAHASGE FDIGGSVASAGSNSNSTVAIDHSIAGEETWAEWTMLNADPARLNANRYNCTGT APIINLVPTSLVTEKROTLTATIKKENQUSQILAPNNRYFSKULAPIALNAODPFESS PTITANNIOFLELETKOURLTDQDVGNIAITYFNENRVRVDGSMSEVLPOIQET TARIIFENGQDLNVERRIRIAAANPSDELTPTPDMTLKALKIATGFENPNLDYOQG DITEEDFPNDQOTSONIKAOALNAVNTIYTVLDKIKLANONMLIRKPRHYRRNNI AAGADEVKKAHREVINSSTEGLLANIIDKDIRKISGYIVEIEBTGLKVINDRYDYD MNISLSRDGKTFPIDPKYNDKILEYISNPYKNVYAATVKENTIIINPSNGDTSTNY GIK"	
BASE COUNT	861 a	328 c 422 g 620 t
ORIGIN		
Query Match	100.0%; Score 23;	DB 1; Length 2231;
Best Local Similarity	100.0%; Pred. No. 3;	
Matches	23; Conservative 0;	Mismatches 0; Indels 0; Gaps 0;
Oy	1 ATGGCGTCGTTCTTGATATTGGT 23	
Dd		
	993 ATGGCTGCITCTTGATATTGGT 1015	
RESULT 10		
AF306778	2369 bp	DNA linear BCT 13-DEC-2000
LOCUS	Bacillus anthracis plasmid px01 protective antigen (pag) gene,	
DEFINITION	complete cds.	
ACCESSION	AF306778	
KEYWORDS	AF306778.1 GI:10880942	

REFERENCE	ORGANISM	SOURCE
JOURNAL	Bacillus anthracis	1 (bases 1 to 2369)
MEDLINE	Bacillus anthracis	Price, L.B., Hugh-Jones, M., Jackson, P.J. and Keim, P.
PubMed	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus	Genetic diversity in the protective antigen gene of Bacillus anthracis
REFERENCE	JOURNAL	1. 2369
TITLE	JOURNAL	2 (bases 1 to 2369)
FEATURES	Source	Price, L.B., Hugh-Jones, M., Jackson, P.J. and Keim, P.
gene	CDs	Direct Submission
CDs	gene	Submitted (20-SEP-2000) Biological Sciences, Northern Arizona University, P.O. Box 5640, Flagstaff, AZ 86011-5640, USA
CDs	CDs	Location/Qualifiers
CDs	CDs	1. 2369
CDs	CDs	/organism="Bacillus anthracis"
CDs	CDs	/mol_type="other DNA"
CDs	CDs	/db_xref="taxon:1392"
CDs	CDs	/plasmid="pX01"
CDs	CDs	1. 2369
CDs	CDs	/gene="pag"
CDs	CDs	49. 2343
CDs	CDs	/gene="pag"
CDs	CDs	/codon_start=1
CDs	CDs	/transl_table=1
CDs	CDs	/product="protective antigen"
CDs	CDs	/protein_id="BA024446.1"
CDs	CDs	/db_xref="GI:10880943"
CDs	CDs	/translation="MKRRKYLIPALMSTLIVSGTNLBYIOAEVKNENLLNSES
CDs	CDs	SOGLGIYISFDLNFQAPMVVTSITGDSIPSELENTPEENOTFOSAINSGTRKVK
CDs	CDs	SDELTAFASADNHTMWDQEVINAKSNRKRLEKGRVYQIKTOGRNPFKRGD
CDs	CDs	PKLWIDQNKKEVTSISDNLQELPELKKSNSSRKRSTAGPTVPDRDNDGIPDSLEV
CDs	CDs	EGVVDVKNKRTFSPWISNTHKEKGLTKYKSPKKSSTAGPYSDPEKVTGRIDKVV
CDs	CDs	SPERHSLFVLAAYPIVHVDMENITLSKEDOSTONDSOTRTISKNTSRTTHSEVGG
CDs	CDs	NAEVAHAFPIGGSVSAQSPNSNSSTVAIDHSLSLAEGRVMAETMGNTADIALNAN
CDs	CDs	IRVYNGTATVAVLPTTSLVIGKNOTLATIKKKNLSOILANNVYPSGNLAPIAL
CDs	CDs	MAODFESTPIYMANVPLELEKTKKQRLDIDOVYGNIAIYVNEGRVVDTSNSEE
CDs	CDs	VLPIQESTTARILFNGKDLNVERLIAVAPSDLETKRDMTKEMKIAFGNENPER
CDs	CDs	GNLDYQKQDITFDPFNFDQOSTONIKQQLAEANNTNITYVLDKIKLAAKNTILRDK
CDs	CDs	FHYDRNIAVGADESVVKAHREYINSTGLNLINDIKRILISGIVAEIETDEGLK
CDs	CDs	EVIDRYDMNLISLRDQGTFFIDPFKYNKXKLPLYISNPYKXVAVYAKENTINPSS
CDs	CDs	ENGDTSTNGIKILIFSKGVEIG"
CDs	CDs	BASE COUNT 924 a 338 c 441 g 666 t
CDs	CDs	ORIGIN
CDs	CDs	Query Match 100.0%; Score 23; DB 1; Length 2369;
CDs	CDs	Best Local Similarity 100.0%; P-adj. No. 3;
CDs	CDs	Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CDs	CDs	1 ATGGCGTCTTGATATGCT 23
CDs	CDs	1064 ATGCGTCTTGATATGCT 1066
CDs	CDs	RESULT 11
CDs	CDs	AF306779 2369 bp DNA linear BCT 13-DEC-2000
CDs	CDs	LOCUS AF306779 2369 bp DNA linear BCT 13-DEC-2000
CDs	CDs	DEFINITION Bacillus anthracis isolate 26 protective antigen (pag) gene,
CDs	CDs	complete cds.
CDs	CDs	AF306779
CDs	CDs	VERSION AF306779.1 GI:10880944
CDs	CDs	KEYWORDS
CDs	CDs	ORGANISM
CDs	CDs	Bacillus anthracis
CDs	CDs	Bacillus anthracis
CDs	CDs	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus
CDs	CDs	cereus group.
CDs	CDs	1 (bases 1 to 2369)
CDs	CDs	Price, L.B., Hugh-Jones, M., Jackson, P.J. and Keim, P.
CDs	CDs	Genetic diversity in the protective antigen gene of Bacillus
CDs	CDs	anthracis





SEQ ID NO: 10

LTATGADIVDTNTKINGINFEKKNKYSISNYMTVDINERPALDNERIKRI  
 QLSPTDPAIGENKTLILORNIIGLEIVDOQIKOSEYVIRIDAKVPSKIDTKIOE  
 AQLINQENKALGLPKYTKLITFNVRNRYASNIYSLILNKNLQSD.IKKVY  
 NYLVGNGRFVFTDITLPTNIAEQYTHODEIYEQVSKGLVPESSRLHLGPKGVEL  
 RNDSGEFIERFGVADVDYAGLIDKNSDVTNSKKRIDIFKEGSGNLTYGRTNAB  
 FFAFAPRLMSTIDHARLKVQKNAKTFQPIINQIKRIINS"

BASE COUNT 987 a 294 c 442 g 695 t  
 ORIGIN

Query Match 100.0%; Score 17; DB 1; Length 2418;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACCTAAGGCTTCGC 17  
 DB 2243 AACCTAAGGCTTCGC 2227

## RESULT 4

LOCUS BACLEFB 3291 bp DNA linear BCT 12-OCT-1995  
 DEFINITION Bacillus anthracis lethal factor (lef) gene, complete cds.  
 ACCESSION M29081.1 GI:143143  
 VERSION M29081.1  
 KEYWORDS anthrax toxin; exotoxin.  
 SOURCE Bacillus anthracis  
 ORGANISM Bacillus anthracis  
 Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus  
 cereus group.  
 1 (bases 1 to 3291)  
 Breig, T.S., and Robertson, D.L.  
 Nucleotide sequence and analysis of the lethal factor gene (lef)  
 from Bacillus anthracis  
 Gene 81 (1), 45-54 (1989)  
 JOURNAL MEDLINE 90034185  
 PUBMED 2509294  
 COMMENT Original  
 FEATURES  
 source Location/Qualifiers  
 1..3291  
 /organism="Bacillus anthracis"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:1392"  
 /clone="pLF74"  
 481..2910  
 /note="lethal factor precursor"  
 /transl\_table=1  
 /codon\_start=1  
 /protein\_id="AA079216.1"  
 /db\_xref="GI:143144"  
 /translation="MTIKKEPIKYSMSCLVTATLISGPVFIPLVQAGHGQVGMAY  
 KEKAKVDENKRDENKTOEHLKIMHIVKIEVGEAAVKAAGKAEGLERKPSD  
 VLEMYKAIGGIYVDDITKHISLEALSDDKKIKDIYKDKALHMHVYAAEGYEP  
 VLIVTQSEDEVYENTEKALNYYEIGKILSDISLKIQQPKELDVLTNKAESDG  
 ODILFTQSLKEHPTDFSEVELEONSNOVQFAFAVYEPHODPLQVAAEAVNY  
 MDKNEOEINLSLELDOORLSRYEKEMIKOYQWMSDSLSEEGGLKICQITIE  
 PKDDIHSLSOEKELKIKIDSSPILSTEREPKTCICIDIRBSISEKELINR  
 IYDSSNPISSEKEPEFKIKLKDQCPYDINORQDITGLIDSSINIDVKKQKRIQ  
 NIDALHOSIGSTINIKIYIENMNINNLATIGADIVDSTDTNKNRNGENEFKNO  
 KYISISNYMTVDINERPALDNERIKRIQSPDRADYENGKLIIGRNGLIKVQV  
 IIKOSEYVIRIDAKVPSKIDTKIOEQLINQENKALGLPKYTKLITFNVRNRY  
 ASNIYSLILNKNLQSD.IKKVYTHODEIYEQVSKGLVPESSRLHLGPKGVEL  
 YEQVSKGLVPESSRLHLGPKGVELRNDSEGFIERFGVADVDYAGLIDKNSD  
 VTNKKRIFDIFKEGSGNLTYGRTNABFAFAPRLMSTIDHARLKVQKNAKTFQPI  
 INQIKRIINS"

REFERENCE 1 (bases 1 to 3291)  
 Breig, T.S., and Robertson, D.L.  
 Nucleotide sequence and analysis of the lethal factor gene (lef)  
 from Bacillus anthracis  
 Gene 81 (1), 45-54 (1989)  
 JOURNAL MEDLINE 90034185  
 PUBMED 2509294  
 COMMENT Original  
 FEATURES  
 source Location/Qualifiers  
 1..3291  
 /organism="Bacillus anthracis"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:1392"  
 /clone="pLF74"  
 481..2910  
 /note="lethal factor precursor"  
 /transl\_table=1  
 /codon\_start=1  
 /protein\_id="AA079216.1"  
 /db\_xref="GI:143144"  
 /translation="MTIKKEPIKYSMSCLVTATLISGPVFIPLVQAGHGQVGMAY  
 KEKAKVDENKRDENKTOEHLKIMHIVKIEVGEAAVKAAGKAEGLERKPSD  
 VLEMYKAIGGIYVDDITKHISLEALSDDKKIKDIYKDKALHMHVYAAEGYEP  
 VLIVTQSEDEVYENTEKALNYYEIGKILSDISLKIQQPKELDVLTNKAESDG  
 ODILFTQSLKEHPTDFSEVELEONSNOVQFAFAVYEPHODPLQVAAEAVNY  
 MDKNEOEINLSLELDOORLSRYEKEMIKOYQWMSDSLSEEGGLKICQITIE  
 PKDDIHSLSOEKELKIKIDSSPILSTEREPKTCICIDIRBSISEKELINR  
 IYDSSNPISSEKEPEFKIKLKDQCPYDINORQDITGLIDSSINIDVKKQKRIQ  
 NIDALHOSIGSTINIKIYIENMNINNLATIGADIVDSTDTNKNRNGENEFKNO  
 KYISISNYMTVDINERPALDNERIKRIQSPDRADYENGKLIIGRNGLIKVQV  
 IIKOSEYVIRIDAKVPSKIDTKIOEQLINQENKALGLPKYTKLITFNVRNRY  
 ASNIYSLILNKNLQSD.IKKVYTHODEIYEQVSKGLVPESSRLHLGPKGVEL  
 YEQVSKGLVPESSRLHLGPKGVELRNDSEGFIERFGVADVDYAGLIDKNSD  
 VTNKKRIFDIFKEGSGNLTYGRTNABFAFAPRLMSTIDHARLKVQKNAKTFQPI  
 INQIKRIINS"

## CDS

sig\_peptide 481..579  
 /note="lethal factor signal peptide"  
 mat\_peptide 580..2907  
 /product="lethal factor"  
 BASE COUNT 1333 a 391 c 564 g 1003 t  
 ORIGIN

Query Match 100.0%; Score 17; DB 1; Length 3291;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AACCTAAGGCTTCGC 17  
 DB 2807 AACCTAAGGCTTCGC 2791

RESULT 5 133395 3291 bp DNA linear PAT 06-FEB-1997  
 LOCUS BACLEFB  
 DEFINITION Sequence 1 from patent US 5591631.  
 ACCESSION 133395  
 VERSION 133395.1 GI:1824186  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 Unclassified.  
 1 (bases 1 to 3291)  
 Leppla, S.H., Klimpel, K.R., Arora, N., Singh, Y., and Nicholas, P.J.  
 Anthrax toxin fusion proteins: nucleic acid encoding same  
 Patent: US 5591631-A 1 07-JAN-1997;  
 FEATURES  
 source Location/Qualifiers  
 1..3291  
 /organism="unknown"

BASE COUNT 1333 a 391 c 564 g 1003 t  
 ORIGIN

Query Match 100.0%; Score 17; DB 6; Length 3291;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACCTAAGGCTTCGC 17  
 DB 2807 AACCTAAGGCTTCGC 2791

RESULT 6 169373 3291 bp DNA linear PAT 04-FEB-1998  
 LOCUS 169373  
 DEFINITION Sequence 1 from patent US 5677274.  
 ACCESSION 169373  
 VERSION 169373.1 GI:2831495  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 Unclassified.  
 1 (bases 1 to 3291)  
 Leppla, S.H., Klimpel, K.R., Arora, N., Singh, Y., and Nicholas, P.J.  
 Anthrax toxin fusion proteins and related methods  
 Patent: US 5677274-A 1 14-OCT-1997;  
 FEATURES  
 source Location/Qualifiers  
 1..3291  
 /organism="unknown"

BASE COUNT 1333 a 391 c 564 g 1003 t  
 ORIGIN

Query Match 100.0%; Score 17; DB 6; Length 3291;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACCTAAGGCTTCGC 17  
 DB 2807 AACCTAAGGCTTCGC 2791

RESULT 7 133395 3631 bp DNA linear BCT 26-APR-1993  
 LOCUS BACLEFB  
 DEFINITION B anthracis plasmid pX01 lethal factor (lef) gene, complete cds.  
 ACCESSION M30210  
 VERSION M30210.1 GI:143141  
 KEYWORDS lethal factor.  
 SOURCE Bacillus anthracis

LTTATGADLVSTDNKXIRNGIFNEFKKFKYSISSNMYIVDINERPALDNRLKRI  
 OLSPTBAGYLENGKILLOBNIGLEIKVOIIOKESEKVIKIDAKVYPSKIDTKIOE  
 AGLNINOMENKALGPKYTKLITPVNHRVSNIVESAYILINEMKNIOSDILKXVT  
 NYLVNNGRFVFTDITLIRINAEQITHCDEIYEOHSGVLYPBERSLILGSPKIBEL  
 KNDSEGFIERGHAVDDYAGTLDKQSDLVTSKTFIDFKESGSMVSYGRTNEAE  
 FFAEAFRLHSTDBARLKVOKNAKPTQPIINDQIKPLINS"

BASE COUNT 987 a 442 g 695 t  
 ORIGIN

Query Match 100.0%; Score 22; DB 1; Length 2418;  
 Best Local Similarity 100.0%; Pred. No. 16;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 ATTAGGATGATGAGGCT 22  
 Db 2043 ATTAGGATGATGAGGCT 2064

# RESULT 4 BACLEFB

LOCUS BACLEFB 3291 bp DNA linear BCT 12-OCT-1995  
 DEFINITION Bacillus anthracis lethal factor (lef) gene, complete cds.  
 ACCESSION M3081  
 VERSION M3081.1 GI:143143  
 KEYWORDS anthrax toxin; exotoxin.  
 SOURCE Bacillus anthracis  
 ORGANISM Bacillus anthracis  
 Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.

REFERENCE 1 (bases 1 to 3291)  
 Bragg, T.S. and Robertson, D.L.  
 Nucleotide sequence and analysis of the lethal factor gene (lef) from Bacillus anthracis  
 Gene 81 (1), 45-54 (1989)  
 JOURNAL MEDLINE 90034185  
 COMMENT PUBMED 2509294  
 FEATURES Original  
 source text: Bacillus anthracis (clone: pLF74) DNA.  
 Location/Qualifiers  
 1..3291  
 /organism="Bacillus anthracis"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:1392"  
 /clone="pLF74"  
 481..2910  
 /note="lethal factor precursor"  
 /codon\_start=1  
 /transl\_table=1  
 /protein\_id="AA079216.1"  
 /db\_xref="GI:143144"  
 /translation="MNIKKEFIKVISMSCLVATILSGRPVLPVQAGSGHGVGMKV  
 KEKKNDEKRDKERBKNQOEHLKEIKRKHVKLEVGKEEVKKEAEKLEVPED  
 VLEWYKAIIGKIIYVDGDIKTHISLEALSEDDKKIKDIYQKALHEHYVAKGYPD  
 VLVLOSSEDYVENTKALNYYEIKILSRDILSKINOPYQKALHEHYVAKGYPD  
 ODLEFTNQKEHPDSEVFELEQNSNEVQVPAKPAAYIEPOHSDVQLAAPPANV  
 MDKNEQEIINSLBELKDOMLSRYEKMKIKOHQWSDSLSEGRILKKLQIPPE  
 PKTDITHSISEKEKIKRQIDSDSPITSEKELKQIDIDPSISEEKILAR  
 IQVDSNPISSEKKEPKIKKIDIDYDINQLODGTGIDSPISINDVRYQYRQDIO  
 NIDALHNSIGSTINIKIYIKENMINNATLUGADVSTNTKNGITNEKRNKQ  
 KYSTISSNMYIVDINERPALDNRLKRIQDSPTRAGYENKILLOBNIGLEIKVO  
 IIOKESEKVIKIDAKVYPSKIDTKIOEAGLVNOMENKALGPKYTKLITPVNHRV  
 ASINIVESAYILINEMKNIOSDILKXVTNYLVNNGRFVFTDITLIRINAEQITHC  
 DEIYEOHSGVLYPBERSLILGSPKIBELKNDSEGFIERGHAVDDYAGTLDKQSDL  
 VEGVHSGVLYPBERSLILGSPKIBELKNDSEGFIERGHAVDDYAGTLDKQSDL  
 VTNSKRFIDIFKEGSMVSYGRTNEAEFRLHSTDBARLKVOKNAKPTQPIINDQIKPLINS"

sig\_peptide  
 /note="lethal factor signal peptide"  
 mat\_peptide 580..2907  
 /product="lethal factor"  
 BASE COUNT 1333 a 391 c 564 g 1003 t  
 ORIGIN  
 Query Match 100.0%; Score 22; DB 1; Length 3291;  
 Best Local Similarity 100.0%; Pred. No. 16;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Cy 1 ATTAGGATGATGAGGCT 22  
 Db 2607 ATTAGGATGATGAGGCT 2628

# RESULT 5

LOCUS 133395 3291 bp DNA linear PAT 06-FEB-1997  
 DEFINITION Sequence 1 from patent US 5591631.  
 ACCESSION 133395  
 VERSION 133395.1 GI:1624186  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.

REFERENCE 1 (bases 1 to 3291)  
 Leppla, S.H., Klimpel, K.R., Arora, N., Singh, Y., and Nicholls, P.J.  
 Anthrax toxin fusion proteins, nucleic acid encoding same  
 Patent: US 5591631-A 1 07-JAN-1997;  
 Location/Qualifiers  
 1..3291  
 /organism="unknown"  
 BASE COUNT 1333 a 391 c 564 g 1003 t  
 ORIGIN

Query Match 100.0%; Score 22; DB 6; Length 3291;  
 Best Local Similarity 100.0%; Pred. No. 16;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 ATTAGGATGATGAGGCT 22  
 Db 2607 ATTAGGATGATGAGGCT 2628

# RESULT 6

LOCUS 169373 3291 bp DNA linear PAT 04-FEB-1998  
 DEFINITION Sequence 1 from patent US 5677274.  
 ACCESSION 169373  
 VERSION 169373.1 GI:2831495  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.

REFERENCE 1 (bases 1 to 3291)  
 Leppla, S.H., Klimpel, K.R., Arora, N., Singh, Y., and Nicholls, P.J.  
 Anthrax toxin fusion proteins and related methods  
 Patent: US 5677274-A 1 14-OCT-1997;  
 Location/Qualifiers  
 1..3291  
 /organism="unknown"  
 BASE COUNT 1333 a 391 c 564 g 1003 t  
 ORIGIN

Query Match 100.0%; Score 22; DB 6; Length 3291;  
 Best Local Similarity 100.0%; Pred. No. 16;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Cy 1 ATTAGGATGATGAGGCT 22  
 Db 2607 ATTAGGATGATGAGGCT 2628

# RESULT 7

LOCUS BACLEF 3631 bp DNA linear BCT 26-APR-1993  
 DEFINITION B.anthraxis plasmid pX01 lethal factor (lef) gene, complete cds.  
 ACCESSION M30210  
 VERSION M30210.1 GI:143141  
 KEYWORDS lethal factor.  
 SOURCE Bacillus anthracis

REC ID NO:12

17ATIGADIVDSTDNKTNRGTFNEFKKPKSSSNMIVDINERPALDNELKXRI  
QUSPTFRAGYELNGKILILORNIIGLEIKVOIIRKSEKEYIRIDAVYKSKIDDKRICE  
AQLNINQEWNKALGLPKTKLITFVNHKNVSNIVESAVILNENKNNISDLIKRT  
NYLVNGNGFVFETDITLNPINAOYTHOBEIYQVHSGKGLYVESSILHGPSSKVEL  
RNDSEGFIEHFGHADVDDYAGYLDKXQSDLVNHSKFLDIFKEBGSNLTYSGRINEAS  
FFAAFPRLMHSSTDHAEKRLKVKQKNAPTFCFINDQIKFTINS"

BASE COUNT 987 a 294 c 442 g 695 t

Query Match 100.0%; Score 22; DB 1; Length 2418;  
Best Local Similarity 100.0%; Pred. No. 2.4;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATACGGAATTGGACATGCT 22  
DB 2067 TATACGGAATTGGACATGCT 2068

RESULT 4  
BACLEB  
LOCUS 3291 bp DNA linear BCT 12-OCT-1995  
DEFINITION Bacillus anthracis lethal factor (lef) gene, complete cds.  
ACCESSION M29081.1 GI:143143  
VERSION M29081.1  
KEYWORDS anthrax toxin; exotoxin.  
SOURCE Bacillus anthracis  
ORGANISM Bacillus anthracis  
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.

REFERENCE 1 (bases 1 to 3291)  
AUTHORS Bragg, J.S. and Robertson, D.L.  
TITLE Nucleotide sequence and analysis of the lethal factor gene (lef) from Bacillus anthracis  
JOURNAL Gene 81 (1), 45-54 (1989)

COMMENT 1  
FEATURES  
source location: Original  
location/Qualifiers  
1..3291  
/organism="Bacillus anthracis"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:1392"  
/clone="pLF74"  
481..2910  
/note="lethal factor precursor"  
/codon\_start=1  
/transl\_table=1  
/protein\_id="AAA79216.1"  
/db\_xref="GI:143144"

CDS

translation="MNITKEFKIVTISGCVTAITLISGPVPIPVQAGGHDVGMHV  
KEKXKQKDEKRNKTOEHEKEMKATVKEVKGAAVKEAENLEKLVAKGIRP  
VLEMYKAGKIVYDGDITRHSLESEKXKIKOYGDALHHEVYAKGIRP  
VLVLOSSEYVETKALNYYEIGKISRDILSKINQYKFLDVAINTTKNADSDG  
ODLFTNOLKEPTDFSVLEFQNSNEVEQFAVAYIIPQHRDYLQAPAFVY  
MDKEBQINLSLETKDQRMISREKEXIKOHQMSDLSSEGGGLKQIQIPLE  
PKKDITHSISOEKEELKRIQIDSSEFLKQIDIRDSISEEKEELNR  
IOWDSSNPLSEKEKFLKKIDTOPYINORLODTGGLDPSINLDPQCYRQDQ  
NIDALLHOSIGSTLTKIYLNNMINNLITLGAADVSTDNKTNRGINRGINERKKNP  
KXISNINMIVDINERPALDNELKRLQLSPTTAGYLENGKILNQNILEKDKQ  
IIKQSEKEYIRIDAVYKSKIDTKIOAQNINQEWNKALGLPKTKLITFVNHKNV  
ASNIVESAVILNENKNNISDLIKRTNYLVNGNGFVFETDITLNPINAOYTHOBEI  
YQVHSGKGLYVESSILHGPSSKVELRNDSEGFIEHFGHADVDDYAGYLDKXQSDL  
VNSKPKFDIEKBSNLTYSGRINEASFFAAFPRLMHSSTDHAEKRLKVKQKNAPTFCF  
INDQIKFTINS"

sig\_peptide 481..579  
mat\_peptide 580..2907  
/note="lethal factor signal peptide"  
/product="lethal factor"

BASE COUNT 1333 a 391 c 564 g 1003 t

Query Match 100.0%; Score 22; DB 1; Length 3291;  
Best Local Similarity 100.0%; Pred. No. 2.4;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TATACGGAATTGGACATGCT 22  
DB 2631 TATACGGAATTGGACATGCT 2652

RESULT 5

LOCUS 13395 3291 bp DNA linear PAT 06-FEB-1997  
DEFINITION Sequence 1 from patent US 5591631.  
ACCESSION 13395  
VERSION 13395.1 GI:1824186  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 3291)  
AUTHORS Leppia, S.H., Klimpel, K.R., Arora, N., Singh, Y. and Nicholls, P.J.  
TITLE Anthrax toxin fusion proteins, nucleic acid encoding same  
JOURNAL Patent: US 5591631-A 1 07-JAN-1997;  
FEATURES location/Qualifiers  
1..3291  
/organism="unknown"

BASE COUNT 1333 a 391 c 564 g 1003 t  
QY 1 TATACGGAATTGGACATGCT 22  
DB 2631 TATACGGAATTGGACATGCT 2652

Query Match 100.0%; Score 22; DB 6; Length 3291;  
Best Local Similarity 100.0%; Pred. No. 2.4;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 6  
LOCUS 169373 3291 bp DNA linear PAT 04-FEB-1998  
DEFINITION Sequence 1 from patent US 5677274.  
ACCESSION 169373  
VERSION 169373.1 GI:2831495  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 3291)  
AUTHORS Leppla, S.H., Klimpel, K.R., Arora, N., Singh, Y. and Nichols, P.J.  
TITLE Anthrax toxin fusion proteins and related methods  
JOURNAL Patent: US 5677274-A 1 14-OCT-1997;  
FEATURES location/Qualifiers  
1..3291  
/organism="unknown"

BASE COUNT 1333 a 391 c 564 g 1003 t  
QY 1 TATACGGAATTGGACATGCT 22  
DB 2631 TATACGGAATTGGACATGCT 2652

Query Match 100.0%; Score 22; DB 6; Length 3291;  
Best Local Similarity 100.0%; Pred. No. 2.4;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 7  
BACLEB 3631 bp DNA linear BCT 26-APR-1993  
LOCUS B.anthraxis plasmid pX01 lethal factor (lef) gene, complete cds.  
DEFINITION M30210  
ACCESSION M30210.1 GI:143141  
VERSION M30210.1  
KEYWORDS lethal factor.  
SOURCE Bacillus anthracis